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(19) **United States**(12) **Patent Application Publication**  
**BIELAS**(10) **Pub. No.: US 2021/0238676 A1**(43) **Pub. Date: Aug. 5, 2021**(54) **COMPOSITIONS AND METHODS FOR  
ACCURATELY IDENTIFYING MUTATIONS**(71) Applicant: **Fred Hutchinson Cancer Research  
Center, Seattle, WA (US)**(72) Inventor: **Jason H. BIELAS, Seattle, WA (US)**(21) Appl. No.: **17/235,750**(22) Filed: **Apr. 20, 2021****Related U.S. Application Data**

(60) Continuation of application No. 16/898,152, filed on Jun. 10, 2020, now abandoned, which is a continuation of application No. 16/657,881, filed on Oct. 18, 2019, now abandoned, which is a continuation of application No. 16/121,555, filed on Sep. 4, 2018, now abandoned, which is a continuation of application No. 15/199,784, filed on Jun. 30, 2016, now Pat. No. 10,450,606, which is a division of application No. 14/378,870, filed on Aug. 14, 2014, now Pat. No. 10,011,871, filed as application No. PCT/US2013/026505 on Feb. 15, 2013.

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(57)

**ABSTRACT**

The present disclosure provides compositions and methods for accurately detecting mutations by uniquely tagging double stranded nucleic acid molecules with dual cyphers such that sequence data obtained from a sense strand can be linked to sequence data obtained from an anti-sense strand when sequenced, for example, by massively parallel sequencing methods.

**Specification includes a Sequence Listing.**